

*B1  
canc'd  
Sub  
C1  
canc'd*

more amino acids an/or substitutions by one or more other amino acids relative to the amino acid sequence described in any one of SEQ ID NOs: 2 through 8 or 12, and still maintains activity of transferring a glycoside to the 5 position of a flavonoid, also belong to the present invention.--

Please replace the paragraph beginning at page 6, line 15, with the following:

*B2  
Sub  
C2*

--The present invention also relates to a gene coding for a protein which gene hybridizes to a nucleotide sequence described in any one of SEQ ID NOs: 1 through 7 or 11, or to a nucleotide sequence that codes for an amino acid sequence described therein or to their portions, for example a portion coding for at least six amino acids of a consensus region, under conditions of 2 to 5 x SSC, and for example, 5 x SSC, and 50°C, and that has activity of transferring a glycoside to the 5 position of a flavonoid. Furthermore, the optimum hybridization temperature varies according to the nucleotide sequence and its length, and it is preferable that the hybridization temperature be lower the shorter the nucleotide sequence. For example, a temperature of 50°C or lower is preferable in the case of a nucleotide sequence (18 bases) coding for six amino acids.--

Please replace the paragraph beginning at page 7, line 1, with the following:

*B3  
Sub  
C3*

--Moreover, the present invention also relates to a gene coding for a protein having an amino acid sequence having homology of 30% or more, preferably 50% or more, for example 60% or 70% or more, and in some cases, 90% or more relative to an amino acid

*B3  
Sub  
C3  
and all*

sequence of any of SEQ ID NOs: 2 through 8 or 12, and having activity that transfers a glycoside to the 5 position of a flavonoid. Namely, as indicated in Example, DNA coding for the enzyme of the present invention demonstrates homology of 20 to 30% in comparison with other glycosyltransferase genes. Thus, the present invention includes genes coding for a protein that having homology of 30% or more with an amino acid sequence described in any one of SEQ ID Nos: 2 through 8 or 12, and has glycosyltransferase activity.--

Please replace the paragraph beginning at page 7, line 15, with the following:

*B3  
Sub  
C3*

--In addition, as is clear from a comparison of the results of Examples 1 through 4, the amino acid sequence of the enzyme of the present invention varies according to the species, with interspecies homology being 50% or more (see Examples 3 and 4), and for example 60 to 70% (see Example 2), while the homology of the amino acid sequences of the enzymes derived from the same species is 90% or more (see Example 1). Thus, genes coding for a protein that has an amino acid sequence having homology of 50% or more, for example 60-70% or more, and in some cases, 90% or more, relative to an amino acid sequence described in any one of SEQ ID NOs: 2 through 8 or 12, and maintains the glycosyltransferase activity of the present invention are included in the present invention.--

Please replace the paragraph beginning at page 8, line 26, with the following:

*B5 Sub C*  
--Alternatively, the protein can be obtained by using antibody to an amino acid sequence described in any one of SEQ ID NOs: 2 through 8 or 12.--

Please replace the paragraph beginning at page 13, line 9, with the following:

*B6*  
--In addition, clones designated as 3R4 and 3R6 were obtained by library screening using the same probes, and these demonstrated an extremely high level of homology with 3R5. The complete nucleotide sequences and deduced amino acid sequences of 3R4 and 3R6 are shown in SEQ ID NO: 1 and SEQ ID NO: 3 of the Sequence Listing, respectively. In addition, the deduced amino acid sequences of the proteins encoded by 3R4 and 3R6 demonstrated homology of 92%.--

Please replace the paragraph beginning at page 17, line 16, with the following:

*B7*  
--The cDNA inserted into pSHGT8 had the length of 2062 bp, and included an open reading frame (ORF) consisting of 1386 bp in length (including a stop codon). This sequence is shown in SEQ ID NO: [3] 5. The amino acid sequence of this ORF had homology of 68% with the amino acid sequence of Perilla 5GT encoded by p3R4, and homology of 64% with that encoded by p3R6. In addition, it also had homology of 22 to 25% with the 3GTs of monocotyledonous and dicotyledoneous plants, and homology of 21% with petunia 3RT.--

Please replace the paragraph beginning at page 19, line 3, with the following:

--The cDNA encoded in pSTGT5 was of 1671 bp in length, and included an open reading frame (ORF) consisting of 1437 bp in length (including a stop codon). This sequence is shown in SEQ ID NO: [4] 7. The amino acid sequence of this ORF had homology of 58% with the amino acid sequence of Perilla 5GT encoded by p3R4, [and] homology of 57% with that encoded by p3R6, and[,] homology of 57% with that encoded by Verbena pSHGT8. In addition, it also had homology of 19 to 23% with the 3GT of monocotyledonous and dicotyledoneous plants, and homology of 20% with petunia 3RT.--

Please replace the paragraph beginning at page 20, line 17, with the following:

--The pSPGT1 cDNA was 2015 bp in length, and included an open reading frame (ORF) consisting of 1407 bp (including a stop codon). This sequence is shown in SEQ ID NO: [6] 11. The amino acid sequence of this ORF had homology of 57% with that of 5GT encoded by p3R4 of Perilla, homology of 54% with that encoded by p3R6, 55% with that encoded by pSHGT8 of verbena, and 51% of that encoded by pTGT5 of torenia. In addition, it also had homology of 20 to 29% with the 3GT of monocotyledonous and dicotyledoneous plants, and homology of 20% with petunia 3RT. Based on this observation, pSPGT1 cDNA obtained from petunia is considered to code for 5GT. --